

FIG. 1A

Input file Fbh18903FL.seq; Output File 18903.trans
Sequence length 1983

CCTTTAGCCAATTGGCCGAGGCCCTCCGCCAGTACTTGCTGGCAGGGATTAAAGGAGATAAAAGGTGTGCTCACAC

	M	P	S	T	V	L	P	S	T	V	L	P	S	L	L	15
P	T	A	G	A	G	W	S	M	R	W	I	L	C	W	S	15
CCC	ACA	GCA	GGA	GCT	GGC	TGG	AGC	ATG	AGG	TGG	ATT	CTG	TGC	TGG	AGC	45
L	M	A	Q	T	A	L	G	A	L	H	T	K	R	P	Q	35
CTG	ATG	GCG	CAG	ACG	GCC	TTG	GGT	GCC	TTG	CAC	ACC	AAG	AGG	CCT	CAA	105
Y	G	T	L	Q	G	K	Q	M	H	V	G	K	T	P	Q	165
TAT	GGA	ACC	CTG	CAA	GGA	AAA	CAG	ATG	CAT	GTG	GGG	AAG	ACA	CCC	ATC	55
G	V	P	F	S	R	P	P	L	G	I	L	R	F	A	P	225
GGA	GTC	CCC	TTC	TCC	AGA	CCT	CCT	CTA	GAT	ATC	CTC	AGG	TTT	GCA	CCT	75
E	P	W	K	G	I	R	D	A	T	T	Y	P	P	E	P	285
GAG	CCC	TGG	AAA	GGA	ATC	AGA	GAT	GCT	ACC	TAC	CCG	CCT	GGG	TGC	CAG	115
W	G	Q	L	A	S	M	Y	V	S	T	R	E	R	Y	K	345
TGG	GGC	CAG	CTG	GCC	TGG	ATG	TAC	GTC	AGC	ACG	CGG	GAA	CGG	TAC	AAG	135
S	E	D	C	L	Y	L	N	V	Y	A	P	A	R	P	G	155
AGC	GAG	GAC	TGT	CTG	TAC	CTG	AAC	GTC	TAC	GCG	CCG	GCG	CGC	GCG	CCC	465
L	P	V	M	V	W	F	P	G	G	A	F	I	V	G	A	175
CTG	CCA	GTG	ATG	GTC	TGG	TTC	CCG	GGA	GGC	GCC	TTC	ATC	GTG	GGC	GCT	525

FIG. 1B

E	G	S	D	L	A	A	R	E	K	V	V	L	V	F	L	Q	H	R	L	195
GAG	GGC	TCT	GAC	TTG	GCC	GCC	CGC	GAG	AAA	GTG	GTG	CTG	GTG	TTT	CTG	CAG	CAC	AGG	CTC	585
G	I	F	G	F	L	S	T	D	D	S	H	A	R	G	N	W	G	L	L	215
GGC	ATC	TTC	GGC	TTC	CTG	AGC	ACG	GAC	GAC	AGC	CAC	GGC	CGC	GGG	AAC	TGG	GGG	CTG	CTG	645
D	Q	M	A	A	L	R	W	V	Q	E	N	I	A	A	F	G	G	D	P	235
GAC	CAG	ATG	GCG	GCT	CTG	CGC	TGG	GTG	CAG	GAG	AAC	ATC	GCA	GCC	TTC	GGG	GGA	GAC	CCA	705
G	N	V	T	L	F	G	Q	S	A	G	A	M	S	I	S	G	L	M	M	255
GGA	AAT	GTG	ACC	CTG	TTC	GGC	CAG	TCG	GCG	GGG	GCC	ATG	AGC	ATC	TCA	GGA	CTG	ATG	ATG	765
S	P	L	A	S	G	L	F	H	R	A	I	S	Q	S	G	T	A	L	F	275
TCA	CCC	CTA	GCC	TCG	GGT	CTC	TTC	CAT	CGG	GCC	ATT	TCC	CAG	AGT	GGC	ACC	GCG	TAA	TTC	825
R	L	F	I	T	S	N	P	L	K	V	A	K	K	V	A	H	L	A	G	295
AGA	CTT	TTC	ATC	ACT	AGT	AAC	CCA	CTG	AAA	GTG	GCC	AAG	AAG	GTT	GCC	CAC	CTG	GCT	GGA	885
C	N	H	N	S	T	Q	I	L	V	N	C	L	R	A	L	S	G	T	K	315
TGC	AAC	CAC	AGC	ACA	CAG	ATC	CTG	GTA	AAC	TGC	CTG	AGG	GCA	CCTA	TCA	GGG	ACC	AAG	945	
V	M	R	V	S	N	K	M	R	F	L	Q	L	N	F	Q	R	D	P	E	335
GTG	ATG	CGT	GTG	TCC	AAC	AAG	ATG	AGA	TTC	CTC	CAA	CTG	AAC	TTC	CAG	AGA	GAC	CCG	GAA	1005
E	I	I	W	S	M	S	P	V	V	D	G	V	V	I	P	D	D	P	L	355
GAG	ATT	ATC	TGG	TCC	ATG	AGC	CCT	GTG	GTG	GAT	GGT	GTG	ATC	CCA	GAT	GAC	CCT	TTC	1065	
V	L	L	T	Q	G	K	V	S	S	V	P	Y	L	L	G	V	N	N	L	375
GTG	CTC	CTG	ACC	CAG	GGG	AAG	GTT	TCA	TCT	GTG	CCC	TAC	CTT	CTA	GGT	GTC	AAC	AAC	CTG	1125
E	F	N	W	L	L	P	Y	I	M	K	F	P	L	N	R	Q	A	M	R	395
GAA	TTC	AAT	TGG	CTC	TTG	CCT	TAT	ATC	ATG	AAG	TTC	CCG	CTA	AAC	CGG	CAG	GCG	ATG	AGA	1185

FIG. 1C

K	E	T	I	T	K	M	L	W	S	T	R	T	L	L	N	I	T	K	E	415	
AAG	GAA	ACC	ATC	ACT	AAG	ATG	CTG	CTC	TGG	AGT	ACC	CGC	ACC	CTG	TTG	AAT	ATC	ACC	AAG	GAG	1245
Q	V	P	L	V	V	E	E	Y	L	D	N	V	N	E	H	D	W	K	M	435	
CAG	GTA	CCA	CTT	GTG	GTG	GAG	GAG	TAC	CTG	GAC	AAT	GTC	AAT	GAG	CAT	GAC	TGG	AAG	ATG	1305	
L	R	N	R	M	M	D	I	V	Q	D	A	T	F	V	Y	A	T	L	Q	455	
CTA	CGA	AAC	CGT	ATG	ATG	GAC	ATA	GTT	CAA	GAT	GCC	ACT	TTC	GTG	TAT	GCC	ACA	CTG	CAG	1365	
T	A	H	Y	H	R	D	A	G	L	P	V	Y	L	Y	E	F	E	H	H	475	
ACT	GCT	CAC	TAC	CAC	CGA	GAT	GCC	GGC	CTC	CCT	GTC	TAC	CTG	TAT	GAA	TTT	GAG	CAC	CAC	1425	
A	R	G	I	I	V	K	P	R	T	D	G	A	D	H	G	D	E	M	Y	495	
GCT	CGT	GGA	ATA	ATC	GTC	AAA	CCC	CGC	ACT	GAT	GGG	GCA	GAC	CAT	GGG	GAT	GAG	ATG	TAC	1485	
F	L	F	G	G	P	F	A	T	G	L	S	M	G	K	E	F	E	H	H	515	
TTC	CTC	TTT	GGG	GGC	CCC	TTC	GCC	ACA	GGC	CTT	TCC	ATG	GGT	AAG	GAG	AAG	GCA	CTT	AGC	1545	
L	Q	M	M	K	Y	W	A	N	F	A	R	T	G	N	P	N	D	G	N	535	
CTC	CAG	ATG	AAA	TAC	TGG	GCC	AAC	TTT	GCC	CGC	ACA	GGA	AAC	CCC	AAT	GAT	GGG	AAT	1605		
L	P	C	W	P	R	Y	N	K	D	E	K	Y	L	Q	L	D	F	T	T	555	
CTG	CCC	TGC	TGG	CCA	CGC	TAC	AAC	AAG	GAT	GAA	AAG	TAC	CTG	CAG	CTG	GAT	TTT	ACC	ACA	1665	
R	V	G	M	K	L	K	E	K	K	M	A	F	W	M	S	L	Y	Q	S	575	
AGA	GTG	GGC	ATG	AAG	CTC	AAG	GAG	AAG	AAG	ATG	GCT	TTT	TGG	ATG	AGT	CTG	TAC	CAG	TCT	1725	
Q	R	P	E	K	Q	R	Q	F	*											585	
CAA	AGA	CCT	GAG	AAG	CAA	TTC	TAA													1755	

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GGGTGGCTATGCCAGGAAGGGCCAAAGAGGGTTTGGCCCCACCATCCAGGGGAATCTGGGAGACTAGCCATGGACATACC
TGGGGACAAGAGTTCTACCCAAAGGGGAATCTGTTAAACCTGGAGGACTAG

FIG. 2

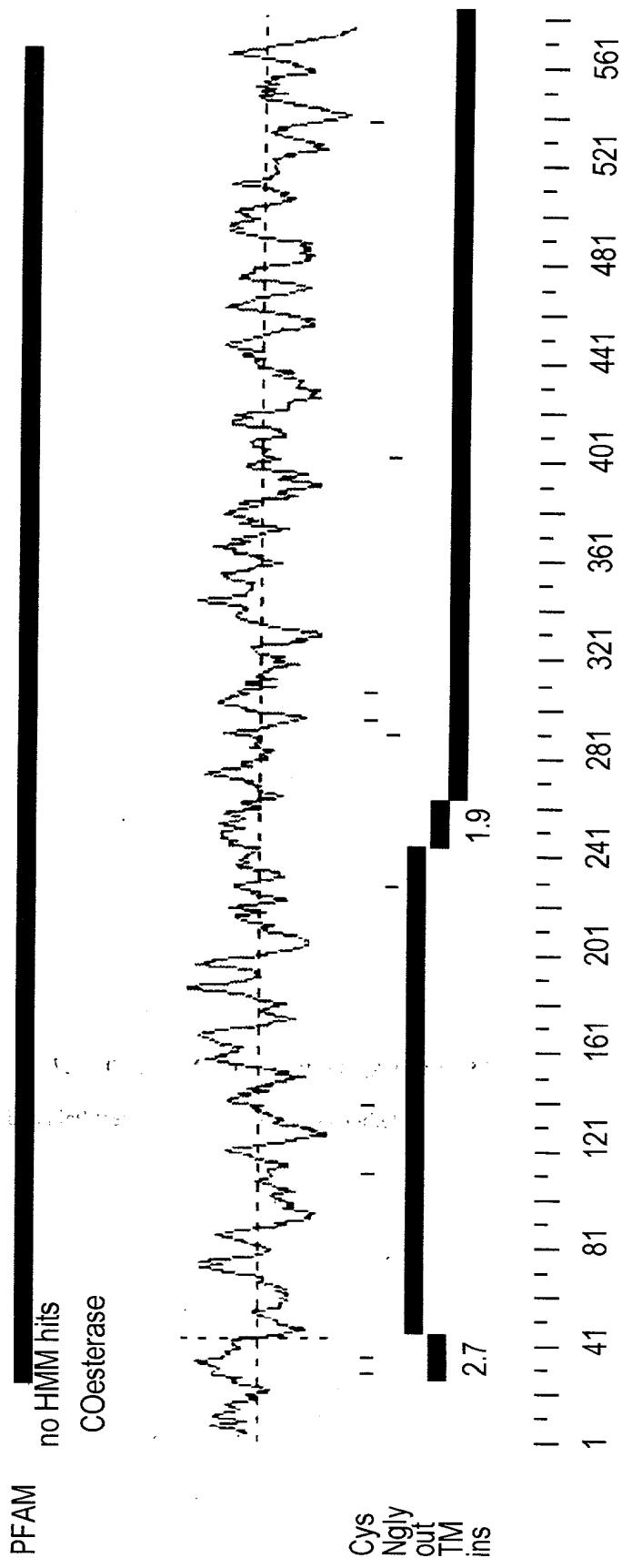


FIG. 3A

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)

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 HMMER is freely distributed under the GNU General Public License (GPL).
 - - - - -
 HMM file: /prod/ddm/seqanal/PFAM/pfam6.4/Pfam
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.6214.seq
 - - - - -
 Query: Fbh18903FL

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
Coesterase	Carboxylesterase	558.6	4.1e-164	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
Coesterase	1/1	25	569 ..	1	612 []	558.6	4.1e-164

Alignments of top-scoring domains:

Coesterase: domain 1 of 1, from 25 to 569: score 558.6, E = 4.1e-164
 *->mvllllflllllliaavlaakaspedpl1VatnnV1cGkvrGvnek
 +1+ +L 1 1 ++ +1+a++ ++ v t++ G++ G++
 18903 25 RWILCWSLTLICLMAQTA1GALHT---KRPQQVVTKY---GTLQGKQMH 65

tdngeqsvsvsF1GIPYAAePPVGnLRFkaPqPYKepWsdv1dAtkypssC1
 + ++ +F1G+P+ PP+G LRF +P+P +epW+++dat+Ypp C1
 18903 66 VGKT--PIQVFLGVPPFSRPPGILRFAPPEP-PEPWKGIRDAATTYPPGCL 112

FIG. 3B

18903	113	Qdddfgfs1sdIKvalkmnlslgwknklvg...1kl1sedCLYLYNvYtPkt Q + +g+ 1 +++ ++ + 1 +sedCLYLYNvY P+ + Q-EStWGQ-----LASMYVSTRERYkwLRFSEDCLYLYNvYAPARA 150	
18903	151	kpnsk1PvmVw1hGGGfmGsghsplslYdgeslaregnVIVVsInYRL + + +1PvmVw +GG+F +G+ +s+Y g+ lat+++v+v ++ RL PGDPQLPVMWFPGGCAFIVGAA-----SSYEGSDLAAREKVVIVFLQHRL 195	
18903	196	Gp1GFLstgddk1pgsGNYGL1DQrlALKWVqdnN1aaFGGDpnsVtIfGe G+GFLst+d++ GN+GL1DQ +AL+WWq+N1aaFGGDp++VT+fG+ GIFGFLSTDDSHAR--GNWGL1DQMAALRWVQENIAAFGGDPGNVTLFGQ 243	
18903	244	SAGaaSVs111sngDnppsskgLFRAISqSGsalspwaqsesnarg SAGA+S+s 1+s p++ qLFRAISqSG+al +i+s+ + SAGAMSIISGIMMS-----PLA-SGFLFRAISQSGTALFRFLITSNP--LK 285	
18903	286	rakellar1lGCnetssselldCLRsksaeeLleatrsfllfeyyvpf1p1f ak++a 1+GCn++s 1+ CLR s + + + + f + +f + VAKKVAHLAGCENNSTQIILVNCLIRALSGCTKVMRVSNK-MRFIQLNQFQDP 334	
18903	335	1.....aFgPvvDGdDapeafipedPeelikeGkfadvPyliGvtkdegqy ++ + +PvvDG+ +ip+dp+ 1+ +Gk + vPy1 Gv++ E+ + EeiwiSMSMSPVVvDGv-----VIPDDPLVLLTQGKVSSVPyLLGVNNLEFMW 379	
18903	380	faamllnasskgdedelkketnpdwlellky1lyfaya sealnikdmddlad +++ +++ + + ket ++ 1+ 11+ + + + LLPYIMKFPPLNR-QAMRKETITK-MLWSTRLLN-ITKEQ-----VP 418	
18903	419	kvlekYpgdvdffsvesrkrpnl1qdm1tD11FkcptrvaadlhakhggsPv v e+Y++ v + + ++ d++ D +F++ + ++ + +g Pv LVVEEYLDNVNEHDWKMLRNRMMDIVQDAtFVYA-TLQTAHYHRDAGLPV 467	

FIG. 3C

		YAYVfdhpasfgigQf1akrvdpeffgavHgdeiffvFgnplkeqlyka
		Y+Y+f h+a+ + v+p+++ga+Hgde++f+Fg p+ ++ 1
18903	468	YLYEFEHHAR-----GIIVKPRTDGADHGDEMFLFCGGPFATG-LS-- 507
		teeeksssktmmywanFAktGnPnngtsng1vrvWppkytseeqkYslli
		@@++s +mm+ywanFA+tGnP n++ +1+ Wp Y+++e +1+
18903	508	MGKEKALLS-LQMMKYWANFARTGNP-NDG--NLPcwPRYNKDEK--YLQL 551
		1lttitaqkllkardprkvlonfw<-*
		+tt +k1k++ +fw
18903	552	DEFTTRVGMKLKEKK-----MAFW 569

//

Searching for complete domains in SMART

FIG. 4A

GAP of: FrGcgManager_76_IOA81nWg_ check: 5132 from: 1 to: 1983

Fbh18903FL - Import - vector trimmed

to: FrGcgManager_76_JOA3WXZ1_ check: 1319 from: 1 to: 2456

z34105 in Patent Nucleotide

Symbol comparison table: /ddm_local/gcg/gcg_9.1/

1/gcgcore/data/rundata/nwsgapdna.cmp

CompCheck: 8760

Gap Weight: 12 Average Match: 10.000
 Length Weight: 4 Average Mismatch: 0.000

Quality: 13796 Length: 2746
 Ratio: 6.957 Gaps: 14
 Percent Similarity: 92.617 Percent Identity: 92.617

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

. = 1

FrGcgManager_76_IOA81nWg_ x FrGcgManager_76_JOA3WXZ1

COE-2 1 CCT 3

Z34105 101 CATTTCGCCTTGCTGACGGCGTCGAGCCCTGGCCAGACATGTCCACAGGG 150
 4 TTAGCCAATT CGGCCGAGGCCTCCGCCAGTA. CTTGCTGGCAGGGAT 52
 151 TTCTCCTTCGGGTCCGGACTCTGGCTCCACCACCGTGGCCGCCGGGG 200
 53 TAAGAGCAGA. TAAAAGTGTGCTCACACACTGTAGACACGGCTACCATGC 101
 201 GACCAGCACAGGCGGGTTTCTCCTTCGGAACGGAACGTCTAGCAACC 250
 102 CATC. CACAGTGTGCCATCCACAGTGTGCCATCACTCCTGC. 143
 251 CTTCTGTGGGGCTCAATTGGAAATCTTGGAAAGTACTTCAACTCCAGCA 300
 144 .CCACAGCAGGAGCT.. GGCTGGAGCATGAGGTGGATTCTGTG.. CTGGA 188
 301 ACTACATCTGCTCCTCAAGTGGTTTGGAACCGGGCTTTGGATCTAA 350

FIG. 4B

FIG. 4C

766 GGTGCAGGAGAACATCGCAGCCTCGGGGGAGACCCAGGAAATGTGACCC 815
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1050 GGTGCAGGAGAACATCGCAGCCTCGGGGGAGACCCAGGAAATGTGACCC 1099
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 816 TGTTCGGCCAGTCGGCGGGGCCATGAGCATCTCAGGACTGATGATGTCA 865
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1100 TGTTCGGCCAGTCGGCGGGGCCATGAGCATCTCAGGACTGATGATGTCA 1149
 . . .
 866 CCCCTAGCCTCGGGTCTCTTCCATCGGCCATTCCCAGAGTGGCACCGC 915
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1150 CCCCTAGCCTCGGGTCTCTTCCATCGGCCATTCCCAGAGTGGCACCGC 1199
 . . .
 916 GTTATTCA GACTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG 965
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1200 GTTATTCA GACTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG 1249
 . . .
 966 TTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC 1015
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1250 TTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC 1299
 . . .
 1016 TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT 1065
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1300 TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT 1349
 . . .
 1066 GAGATTCTCCA ACTGA ACTTCCAGAGAGACCCGGAAGAGATTATCTGGT 1115
 ||||| ||||| ||||| ||||| ||||| |||||
 1350 GAGATTCTCCA ACTGA ACTTCCAGAGAGACCCGGAAGAGATTATCTGGT 1399
 . . .
 1116 CCATGAGCCCTGTGGTGGATGGTGTGGT GATCCCAGATGACCCTTGGT 1165
 ||||| ||||| ||||| ||||| ||||| |||||
 1400 CCATGAGCCCTGTGGTGGATGGTGTGGT GATCCCAGATGACCCTTGGT 1449
 . . .
 1166 CTCCTGACCCAGGGGAAGGTTCATCTGTGCCCTACCTCTAGGTGTCAA 1215
 ||||| ||||| ||||| ||||| ||||| |||||
 1450 CTCCTGACCCAGGGGAAGGTTCATCTGTGCCCTACCTCTAGGTGTCAA 1499
 . . .
 1216 CAACCTGGAATTCAATTGGCTTTGCCTTATATCATGAAGTTCCCGCTAA 1265
 ||||| ||||| ||||| |||||
 1500 CAACCTGGAATTCAATTGGCTTTGCCTTAT..... 1530
 . . .
 1316 CGCACCCCTGTTGAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGA 1365
 ||||| ||||| ||||| ||||| ||||| |||||
 1531AATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGA 1568
 . . .
 1366 GTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTA 1415

FIG. 4D

1416 TGATGGACATAGTTCAAGATGCCACTTCGTGTATGCCACACTGCAGACT 1465
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1619 TGATGGACATAGTTCAAGATGCCACTTCGTGTATGCCACACTGCAGACT 1668
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1466 GCTCACTACCACCGAGATGCCGGCTCCCTGTCTACCTGTATGAATTGA 1515
 ||||||| ||||||| |||||
 1669 GCTCACTACCACCGA..... 1683

1666 CAACTTGCCCCCACAGGAAACCCAATGATGGGAATCTGCCCTGCTGGC 1715
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1684GAAACCCAATGATGGGAATCTGCCCTGCTGGC 1716
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1716 CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTACCACAAGA 1765
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1717 CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTACCACAAGA 1766
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1766 GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTGGATGAGTCTGTA 1815
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1767 GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTGGATGAGTCTGTA 1816
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1816 CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA 1865
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1817 CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA 1866
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1866 GGAAGGAGCCAAAGAGGGTTGCCCTACCATCCAGGCCCTGGGAGAC 1915
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1867 GGAAGGAGCCAAAGAGGGTTGCCCTACCATCCAGGCCCTGGGAGAC 1916
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1916 TAGCCATGGACATACCTGGGACAAGAGTTCTACCCAAAGGGCGAATTG 1965
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1917 TAGCCATGGACATACCTGGGACAAGAGTTCTACCC...CCCCA...GT 1960
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 1966 TAAACCTGCAGGA.CTAG..... 1983
 ||||| ||||||| |||||
 1961 TTAGAACTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTT 2010

FIG. 5A

ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
 COE-2 584 aa vs.
 PRO873 545 aa
 scoring matrix: BLOSUM50, gap penalties: -12/-2
 62.4% identity; Global alignment score: 2271

FIG. 5B

1.60	170	180	190	200	210
COE-2	VWFPGGAFIVGAASSYEGSDLAAAREKVVLVFLQHRLGIGFGFLSTDDSHARGNWGLLDQMA				
pro873	VWFPGGAFIVGAASSYEGSDLAAAREKVVLVFLQHRLGIGFGFLSTDDSHARGNWGLLDQMA				
	250	260	270	280	290
	300	310	320	330	340
	350	360	370	380	390
	400	410	420	430	440
	450	460	470	480	490
	500	510			
220	230	240	250	260	270
COE-2	ALRWQENTIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRASQS GTALFR LFI				
pro873	ALRWQENTIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRASQS GTALFR LFI				
	310	320	330	340	350
	360	370	380	390	400
	410	420	430	440	450
	460	470	480	490	500
280	290	300	310	320	330
COE-2	TSNPLKVAHLAGCNHNSTQILVNCLRA LSGTKVMRVS N KMRFLQLN FQ RDPEEJ I W				
pro873	TSNPLKVAHLAGCNHNSTQILVNCLRA LSGTKVMRVS N KMRFLQLN FQ RDPEEJ I W				
	370	380	390	400	410
	420	430	440	450	460
	470	480	490	500	
340	350	360	370	380	390
COE-2	SMS P VVDG VVIPDDPLVLLTQGK VSSV PYLLGVNNL EFNWL L P YIMK FPLN RQAMRKETI				
pro873	SMS P VVDG VVIPDDPLVLLTQGK VSSV PYLLGVNNL EFNWL L P YIMK FPLN RQAMRKETI				
	430	440	450	460	470
	480	490	500		

FIG. 5C

460	470	480	490	500	510
COE-2	HRDAGLPPVYLYEFFEHARGITIVKPRTDGADHGDEMFLGGPFATGLSMGKEKALSILQMM				
:	:	:	:	:	:
pro873	HRET--PMM-----GIC--P----AGHA-----				
520					
520	530	540	550	560	570
COE-2	KYWANFARTGNPNNDGNLPCWPRYNKDEKYLQLDFITTRVGMLKKEKRMMAFWMSLYQSQRPE				
pro873	-	-	-	-	-
530					
540					
580					
COE-2	KQRQF				
pro873	-QEWA				

FIG. 6A

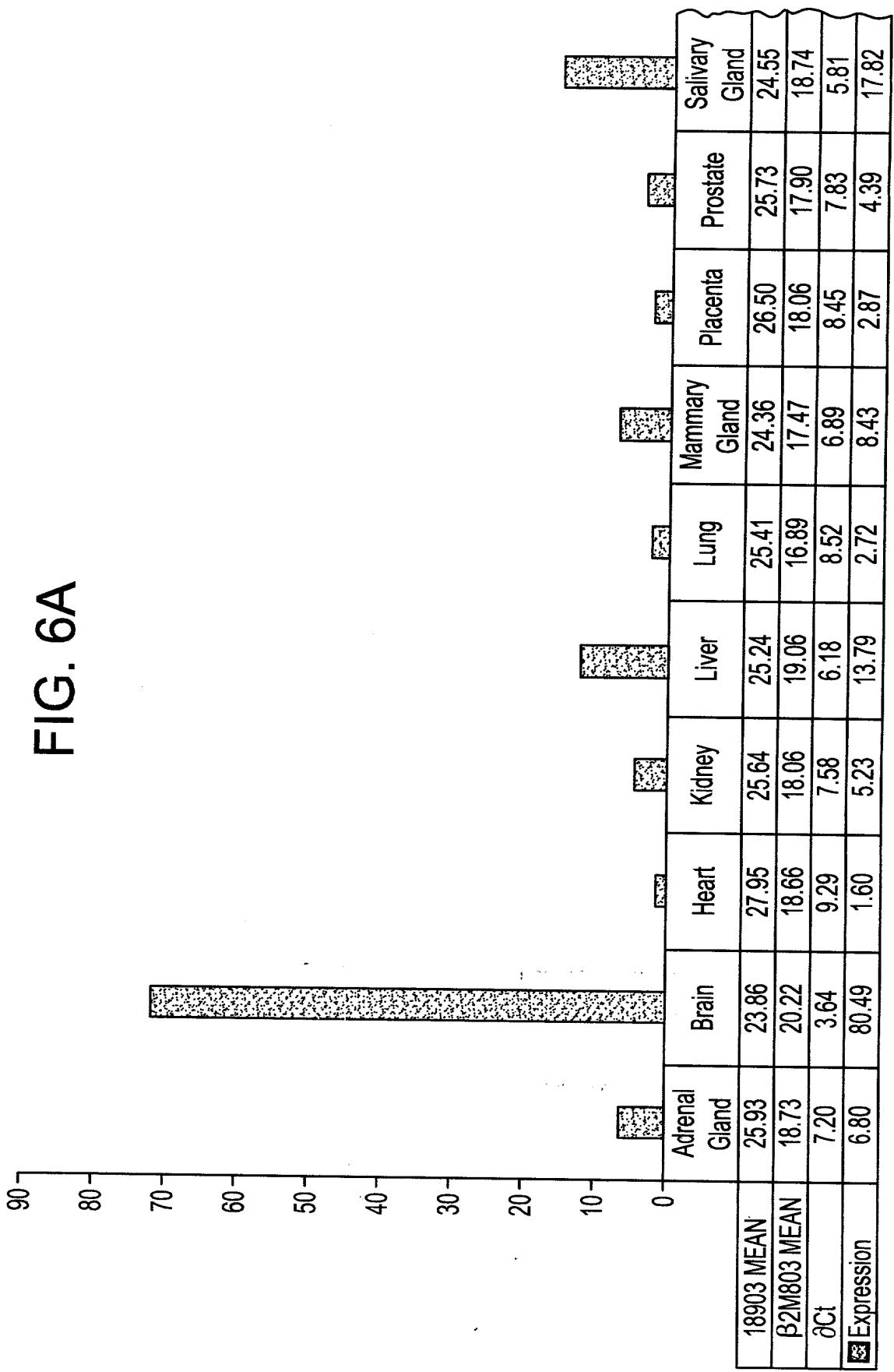
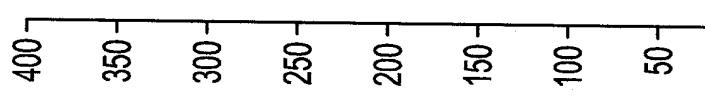


FIG. 6B

Muscle	Sm. Intestine	Spleen	Stomach	Teste	Thymus	Trachea	Uterus	Spinal Cord	Skin	DRG
29.70	25.43	26.89	26.27	24.29	26.33	25.14	26.18	23.99	23.01	25.06
20.66	17.86	16.37	18.03	19.32	18.19	19.10	18.53	19.20	17.10	19.07
9.04	7.58	10.52	8.25	4.97	8.15	6.04	7.66	4.80	5.91	5.99
1.91	5.24	0.68	3.30	31.91	3.53	15.25	4.96	36.02	16.63	15.73

FIG. 7A



	MK cortex	MK DRG	MK spinal cord	MK sciatic nerve	MK kidney	MK hairy skin	MK heart	MK gastro	MK muscle	MK liver
18903 Average Ct	36.935	40	35.89	40	33.735	36.89	37.44	37.235	27.39	
HK Average Ct	20.365	17.375	18.71	17.37	17.78	18.295	17.655	18.91	18.22	
delta Ct	16.57	22.625	17.18	22.63	15.955	18.595	19.785	18.325	9.17	
Relative Expression	0.01579689	0.00023759	0.01035007	0.00023677	0.02419385	0.00388138	0.00170122	0.0046802	2.66804738	

FIG. 7B

	Hu. Brain	Hu. Spinal cord	Hu. Heart	Hu. Kidney	Hu. Liver	Hu. Lung
21.27	23.78	28.26	26.155	25.43	25.805	
19.245	18.295	17.855	17.925	18.22	15.87	
2.025	5.485	10.405	8.23	7.21	9.935	
377.618146	34.3154004	1.13349992	5.11872423	10.3803579	1.57002147	

FIG. 8A-1

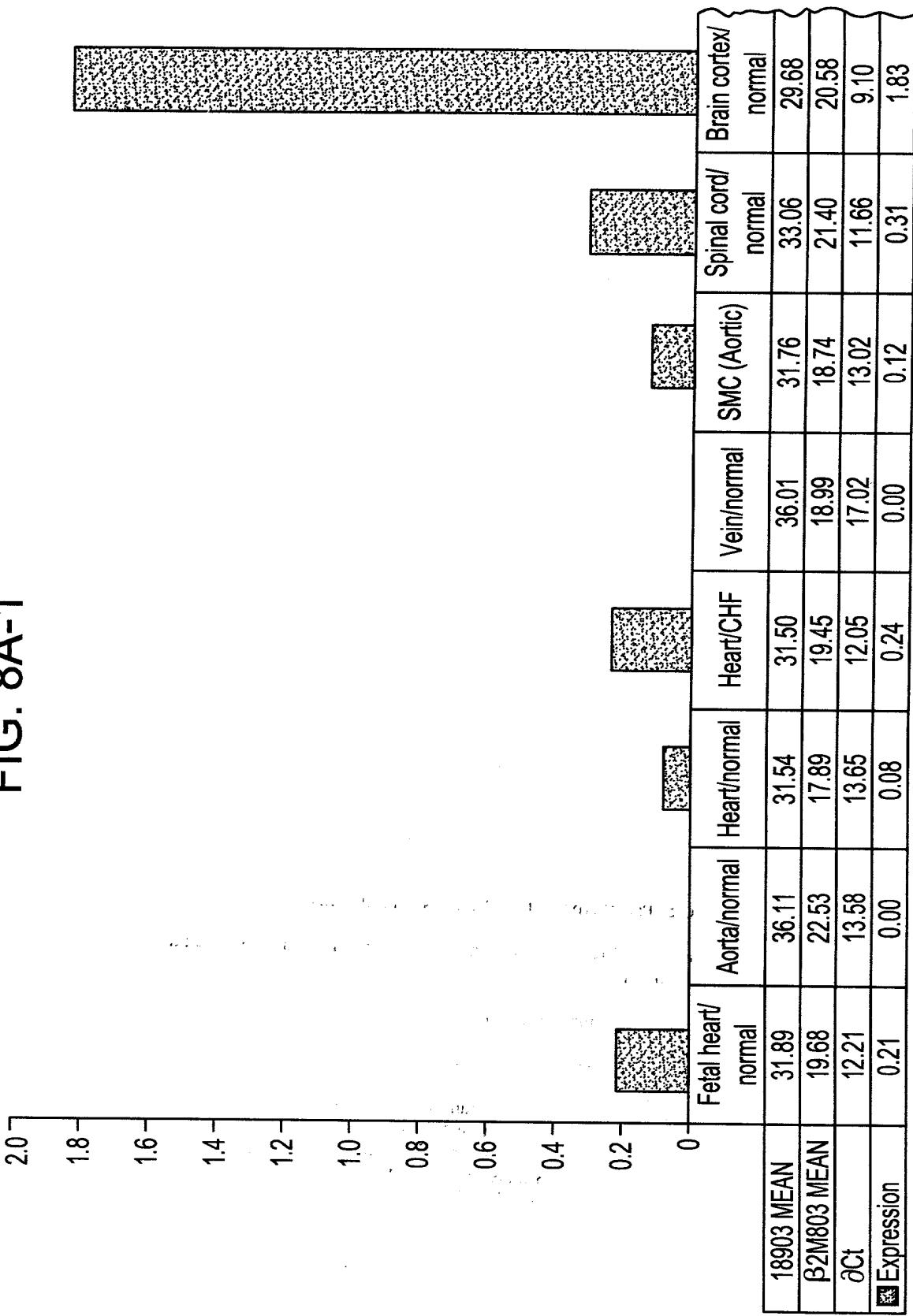


FIG. 8A-2

Brain	Glia cells (Astrocytes)	Brain/ Glioblastoma	Breast/ normal	Breast tumor/ IDC	OVARY/ Normal	OVARY/ Tumor	Pancreas	Prostate/ Normal	Prostate/ Tumor
29.45	33.94	30.39	30.10	30.75	31.73	33.59	30.88	31.16	29.03
19.24	21.09	17.43	18.60	17.66	19.95	18.91	17.33	18.34	17.57
10.21	12.86	12.97	11.50	13.09	11.79	14.68	13.55	12.83	11.46
0.85	0.13	0.13	0.35	0.11	0.28	0.04	0.08	0.14	0.35

FIG. 8A-3

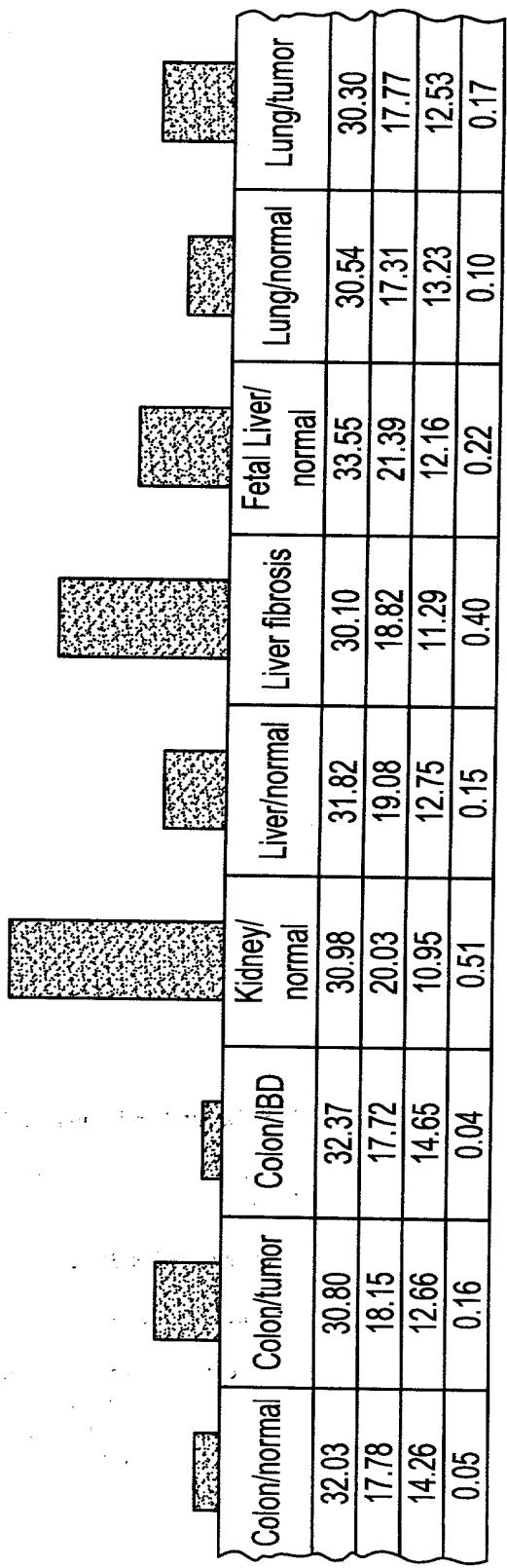


FIG. 8A-4

Lung/COPD	Tonsil/normal	Lymph node/normal	Thymus/normal	Epithelial Cells (Prostate)	Endothelial Cells (Aortic)	Skeletal Muscle	Fibroblasts (Dermal)	Skin/Normal	Adipose/Normal
29.44	31.13	31.40	32.80	30.70	35.27	31.06	33.10	31.16	32.43
17.10	17.19	17.91	20.03	20.13	20.16	18.26	18.18	20.29	17.96
12.34	13.94	13.49	12.78	10.57	15.11	12.81	14.92	10.87	14.47
0.19	0.06	0.09	0.14	0.66	0.03	0.14	0.03	0.54	0.04

FIG. 8A-5

	Osteoblasts (Primary)	Osteoblasts (Undiff)	Osteoblasts (Diff)	Osteoclasts	Aorta SMC (Early)	Aorta SMC (Late)	HUVEC	HMVEC
34.84	33.19	33.23	32.47	32.50	32.72	32.17	32.74	
20.44	18.50	17.83	17.25	19.53	18.77	19.27	18.74	
14.40	14.69	15.40	15.22	12.97	13.96	12.91	14.00	
0.05	0.04	0.02	0.03	0.13	0.06	0.13	0.06	

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FIG. 8B

Tissue	18903 MEAN	β 2M803 MEAN	δ Ct	Expression
Fetal heart/normal	31.89	19.68	12.21	0.21
Aorta/normal	36.11	22.53	13.58	0.00
Heart normal	31.54	17.89	13.65	0.08
Heart/CHF	31.50	19.45	12.05	0.24
Vein/normal	36.01	18.99	17.02	0.00
SMC (Aortic)	31.76	18.74	13.02	0.12
Spinal cord/normal	33.06	21.40	11.66	0.31
Brain cortex/normal	29.68	20.58	9.10	1.83
Brain hypothalamus/normal	29.45	19.24	10.21	0.85
Glial cells (Astrocytes)	33.94	21.09	12.86	0.13
Brain/Glioblastoma	30.39	17.43	12.97	0.13
Breast/normal	30.10	18.60	11.50	0.35
Breast tumor/IDC	30.75	17.66	13.09	0.11
Ovary/normal	31.73	19.95	11.79	0.28
Ovary/tumor	33.59	18.91	14.68	0.04
Pancreas	30.88	17.33	13.55	0.08
Prostate/normal	31.16	18.34	12.83	0.14
Prostate/tumor	29.03	17.57	11.46	0.35
Colon/normal	32.03	17.78	14.26	0.05
Colon/tumor	30.80	18.15	12.66	0.16
Colon/IBD	32.37	17.72	14.65	0.04
Kidney/normal	30.98	20.03	10.95	0.51
Liver/normal	31.82	19.08	12.75	0.15
Liver/fibrosis	30.10	18.82	11.29	0.40
Fetal Liver/normal	33.55	21.39	12.16	0.22
Lung/normal	30.54	17.31	13.23	0.10
Lung/tumor	30.30	17.77	12.53	0.17
Lung/COPD	29.44	17.10	12.34	0.19
Tonsil/normal	31.13	17.19	13.94	0.06
Lymph node/normal	31.40	17.91	13.49	0.09
Thymus/normal	32.80	20.03	12.78	0.14
Epithelial Cells(prostate)	30.70	20.13	10.57	0.66
Endothelial Cells(aortic)	35.27	20.16	15.11	0.03
Skeletal Muscle/normal	31.06	18.26	12.81	0.14
Fibroblasts (Dermal)	33.10	18.18	14.92	0.03
Skin/normal	31.16	20.29	10.87	0.54
Adipose/normal	32.43	17.96	14.47	0.04
Osteoblasts (primary)	34.84	20.44	14.40	0.05
Osteoblasts (Undiff)	33.19	18.50	14.69	0.04
Osteoblasts (Diff)	33.23	17.83	15.40	0.02
Osteoblasts	32.47	17.25	15.22	0.03
Aorta SMC (Early)	32.50	19.53	12.97	0.13
Aorta SMC (Late)	32.72	18.77	13.96	0.06
HUVEC	32.17	19.27	12.91	0.13
HMVEC	32.74	18.74	14.00	0.06
	40.00	40.00	0.00	